

1

SEQUENZPROTOKOLL

<110> Deutsches Krebsforschungszentrum

<120> Fv-Antikörper-Konstrukte

<130> K 2839

<140> unbekannt

<150> DE 199 37 264.0

<151> 1999-08-06

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 4570

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen
Sequenz: Expressionsvektor kodierend für zwei
einkettige Fv-Antikörper-Konstrukte

<220>

<221> CDS

<222> (217)..(1002)

<220>

<221> CDS

<222> (1102)..(1920)

<400> 1

```

ctcgagagcg ggcagtgagc gcaacgcaat taatgtgagt tagctcactc attaggcacc 60
ccaggcttta cactttatgc tcccggctcg tatgttgtgt ggaattgtga gcggataaca 120
atttcacaca gaattcatta aagaggagaa attaaccatg aaatacctat tgcctacggc 180
agccgctggc ttgctgctgc tggcagctca gccgcc atg gcg cag gtg cag ctg 234
                               Met Ala Gln Val Gln Leu
                               1           5

cag cag tct gga gct gag ctg gta agg cct ggg act tca gtg aag ata 282
Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser Val Lys Ile
                10                15                20

tcc tgc aag gct tct ggc tac acc ttc act aac tac tgg cta ggt tgg 330
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Trp Leu Gly Trp
                25                30                35

gta aaa cag agg cct gga cat gga ctc gag tgg att gga gat atc tac 378
Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly Asp Ile Tyr
                40                45                50

cct gga ggt ggt tat act aac tac aat gag aaa ttc aag ggc aag gcc 426
Pro Gly Gly Gly Tyr Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala
                55                60                65                70

```

aca gtg act gca gac aca tcc tcc aga act gcc tac gtg cag gtc agg	474
Thr Val Thr Ala Asp Thr Ser Ser Arg Thr Ala Tyr Val Gln Val Arg	
75 80 85	
agc ctg aca tct gag gac tct gct gtc tat ttc tgt gca aga tcg gct	522
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Ser Ala	
90 95 100	
agc tgg tac ttc gat gtc tgg ggc gca cgg act acg gtc acc gtc tcc	570
Ser Trp Tyr Phe Asp Val Trp Gly Ala Arg Thr Thr Val Thr Val Ser	
105 110 115	
tca gcc aaa aca aca ccc aag ctt ggc ggt gat atc gag ctc act cag	618
Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile Glu Leu Thr Gln	
120 125 130	
tct cca aaa ttc atg tcc aca tca gta gga gac agg gtc aac gtc acc	666
Ser Pro Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Asn Val Thr	
135 140 145 150	
tac aag gcc agt cag aat gtg ggt act aat gta gcc tgg ttt caa caa	714
Tyr Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Phe Gln Gln	
155 160 165	
aaa cca ggg caa tct cct aaa gtt ctg att tac tcg gca tct tac cga	762
Lys Pro Gly Gln Ser Pro Lys Val Leu Ile Tyr Ser Ala Ser Tyr Arg	
170 175 180	
tac agt gga gtc cct gat cgc ttc aca ggc agt gga tct gga aca gat	810
Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp	
185 190 195	
ttc act ctc acc atc agc aat gtg cag tct gaa gac ttg gca gag tat	858
Phe Thr Leu Thr Ile Ser Asn Val Gln Ser Glu Asp Leu Ala Glu Tyr	
200 205 210	
ttc tgt cag caa tat cac acc tat cct ctc acg ttc gga ggg ggc acc	906
Phe Cys Gln Gln Tyr His Thr Tyr Pro Leu Thr Phe Gly Gly Gly Thr	
215 220 225 230	
aag ctg gaa atc aaa cgg gct gat gct gcg gcc gct gga tcc gaa caa	954
Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Ala Ala Gly Ser Glu Gln	
235 240 245	
aag ctg atc tca gaa gaa gac cta aac tca cat cac cat cac cat cac	1002
Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His His His His	
250 255 260	
taaagatcta ttaaagagga gaaattaacc atgaaatacc tattgcctac ggcagccgct	1062
ggcttgctgc tgctggcagc tcagccggcc atggcggcc atg gcc cag gtg caa	1116
Met Ala Gln Val Gln	
265	
ctg cag cag tca ggg gct gag ctg gct aga cct ggg gct tca gtg aag	1164
Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys	
270 275 280	
atg tcc tgc aag gct tct ggc tac acc ttt act acc tac aca ata cac	1212
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr Thr Ile His	
285 290 295	
tgg gta aga cag agg cct gga cac gat ctg gaa tgg att gga tac att	1260
Trp Val Arg Gln Arg Pro Gly His Asp Leu Glu Trp Ile Gly Tyr Ile	
300 305 310 315	

aat cct agc agt gga tat tct gac tac aat cag aac ttc aag ggc aag	1308
Asn Pro Ser Ser Gly Tyr Ser Asp Tyr Asn Gln Asn Phe Lys Gly Lys	
320 325 330	
acc aca ttg act gca gac aag tcc tcc aac aca gcc tac atg caa ctg	1356
Thr Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr Met Gln Leu	
335 340 345	
aac agc ctg aca tct gag gac tct gcg gtc tat tac tgt gca aga aga	1404
Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Arg	
350 355 360	
gcg gac tat ggt aac tac gaa tat acc tgg ttt gct tac tgg ggc caa	1452
Ala Asp Tyr Gly Asn Tyr Glu Tyr Thr Trp Phe Ala Tyr Trp Gly Gln	
365 370 375	
ggg acc acg gtc acc gtc tcc tca gcc aaa aca aca ccc aag ctt ggc	1500
Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly	
380 385 390 395	
ggt gat atc cag gct gtt gtg act cag gaa tct gca ctc acc aca tca	1548
Gly Asp Ile Gln Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser	
400 405 410	
cct ggt gaa aca gtc aca ctc act tgt cgc tca aat act ggg act gtt	1596
Pro Gly Glu Thr Val Thr Leu Thr Cys Arg Ser Asn Thr Gly Thr Val	
415 420 425	
aca act agt aac tat gcc aac tgg gtc caa gaa aaa cca gat cat tta	1644
Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu	
430 435 440	
ttc act ggt cta ata ggt cat acc aac aac cga gct cca ggt gtt cct	1692
Phe Thr Gly Leu Ile Gly His Thr Asn Asn Arg Ala Pro Gly Val Pro	
445 450 455	
gcc aga ttc tca ggc tcc ctg att gga gac aag gct gcc ctc acc atc	1740
Ala Arg Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile	
460 465 470 475	
aca ggg gca cag act gag gat gag gca ata tat ttc tgt gct cta tgg	1788
Thr Gly Ala Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp	
480 485 490	
tat aac aac cat tgg gtg ttc ggt gga gga acc aaa ctg act gtc cta	1836
Tyr Asn Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu	
495 500 505	
ggc cag ccc aag tct gcg gcc gct gga tcc gaa caa aag ctg atc tca	1884
Gly Gln Pro Lys Ser Ala Ala Ala Gly Ser Glu Gln Lys Leu Ile Ser	
510 515 520	
gaa gaa gac cta aac tca cat cac cat cac cat cac taatctagag	1930
Glu Glu Asp Leu Asn Ser His His His His His His	
525 530 535	
gcctgtgcta atgatcagct agcttgaggc atcaataaaa cgaaaggctc agtcgaaaga	1990
ctgggccttt cgttttatct gttgtttgtc gggttaacgtc gacctggcgt aatagcgaga	2050
ggcccgacc gatcgccctt cccaacagtt gcgcagcctg aatggcgaat gggacgcgcc	2110
ctgtagcggc gcattaagcg cggcgggtgt ggtggttacg cgcagcgtga ccgtacact	2170
tgccagcgcc ctagcgcccg ctcttttcgc ttttttccct tcctttctcg ccacgttcgc	2230
cggttttccc cgtcaagctc taaatcgagg gctcccttta gggttccgat ttagtgcttt	2290

acggcacctc gacccccaaa aacttgatta ggggtgatggg tcacgtagtg ggccatcgcc 2350
 ctgatagacg gtttttcgcc ctttgacgtt ggagtcacg ttctttaata gtggactcct 2410
 gttccaaact ggaacaacac tcaaccctat ctcgggtctat tcttttgatt tataagggat 2470
 tttgccgatt tcggcctatt ggttaaaaaa tgagctgatt taacaaaaat ttaacgcgaa 2530
 ttttaacaaa atattaacgc ttacaattta ggtggcactt ttcggggaaa tgtgcgcgga 2590
 acccctattt gtttattttt ctaaatacat tcaaatatgt atccgctcat gagacaataa 2650
 ccctgataaa tgcttcaata atattgaaaa aggaagagta tgagtattca acatttcctg 2710
 gtcgccctta ttcccttttt tgcggcattt tgcccttcctg tttttgctca cccagaaacg 2770
 ctggtgaaag taaaagatgc tgaagatcag ttgggtgcac gagtgggtta catcgaactg 2830
 gatctcaaca gcggtgaagat ccttgagagt tttcgccccg aagaacgttt tccaatgatg 2890
 agcactttta aagttctgct atgtggcgcg gtattatccc gtattgacgc cgggcaagag 2950
 caactcggtc gccgcataca ctattctcag aatgacttgg ttgagtactc accagtcaca 3010
 gaaaagcatc ttacggatgg catgacagta agagaattat gcagtgtgc cataaccatg 3070
 agtgataaca ctgcggccaa cttacttctg acaacgatcg gaggaccgaa ggagctaacc 3130
 gcttttttgc acaacatggg ggatcatgta actcgccttg atcgttggga accggagctg 3190
 aatgaagcca taccaaacga cgagcgtgac accacgatgc ctgtagcaat ggcaacaacg 3250
 ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca attaatagac 3310
 tggatggagg cggataaagt tgcaggacca cttctgcgct cggcccttcc ggctggctgg 3370
 tttattgctg ataaatctgg agccggtgag cgtgggtctc gcggtatcat tgcagcactg 3430
 gggccagatg gtaagccctc ccgtatcgta gttatctaca cgacggggag tcaggcaact 3490
 atggatgaac gaaatagaca gatcgctgag ataggtgcct cactgattaa gcattggtaa 3550
 ctgtcagacc aagtttactc atatatactt tagattgatt taaaacttca tttttaattt 3610
 aaaaggatct aggtgaagat cttttttgat aatctcatga ccaaatccc ttaacgtgag 3670
 ttttcgttcc actgagcgtc agaccccgta gaaaagatca aaggatcttc ttgagatcct 3730
 ttttttctgc gcgtaatctg ctgcttgcaa acaaaaaaac caccgtacc agcggtggtt 3790
 tgtttgcgg atcaagagct accaactctt tttccgaagg taactggctt cagcagagcg 3850
 cagataccaa atactgtcct tctagtgtag ccgtagttag gccaccactt caagaactct 3910
 gtagcaccgc ctacatacct cgctctgcta atcctgttac cagtggctgc tgccagtggc 3970
 gataagtcgt gtcttaccgg gttggactca agacgatagt taccggataa ggcgcagcgg 4030
 tcgggctgaa cgggggggtc gtgcacacag cccagcttgg agcgaacgac ctacaccgaa 4090
 ctgagaacct acagcgtgag ctatgagaaa gcgccacgct tcccgaaggg agaaaggcgg 4150
 acaggtatcc ggtaagcggc agggtcggaa caggagagcg cacgaggag cttccagggg 4210
 gaaacgcctg gtatctttat agtctgtcgg ggtttcgcca cctctgactt gagegtcgat 4270
 ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa cgccagcaac gcggcctttt 4330

<400> 2

```
<210> 3
<211> 273
<212> PRT
<213> Künstliche Sequenz
<223> Beschreibung der künstlichen
Sequenz: Expressionsvektor kodierend für zwei
einkettige Fv-Antikörper-Konstrukte
```

<400> 3

Met	Ala	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Ala	Arg	Pro
1				5					10					15	
Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr
		20						25					30		
Thr	Tyr	Thr	Ile	His	Trp	Val	Arg	Gln	Arg	Pro	Gly	His	Asp	Leu	Glu
		35					40					45			
Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Ser	Ser	Gly	Tyr	Ser	Asp	Tyr	Asn	Gln
	50					55					60				
Asn	Phe	Lys	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Asn	Thr
65					70					75					80
Ala	Tyr	Met	Gln	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr
			85						90					95	
Tyr	Cys	Ala	Arg	Arg	Ala	Asp	Tyr	Gly	Asn	Tyr	Glu	Tyr	Thr	Trp	Phe
		100						105					110		
Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Lys	Thr
		115					120					125			
Thr	Pro	Lys	Leu	Gly	Gly	Asp	Ile	Gln	Ala	Val	Val	Thr	Gln	Glu	Ser
	130					135					140				
Ala	Leu	Thr	Thr	Ser	Pro	Gly	Glu	Thr	Val	Thr	Leu	Thr	Cys	Arg	Ser
145					150					155					160
Asn	Thr	Gly	Thr	Val	Thr	Thr	Ser	Asn	Tyr	Ala	Asn	Trp	Val	Gln	Glu
			165						170					175	
Lys	Pro	Asp	His	Leu	Phe	Thr	Gly	Leu	Ile	Gly	His	Thr	Asn	Asn	Arg
		180						185					190		
Ala	Pro	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Leu	Ile	Gly	Asp	Lys
		195					200					205			
Ala	Ala	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Thr	Glu	Asp	Glu	Ala	Ile	Tyr
	210					215					220				
Phe	Cys	Ala	Leu	Trp	Tyr	Asn	Asn	His	Trp	Val	Phe	Gly	Gly	Gly	Thr
225					230					235					240
Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ser	Ala	Ala	Ala	Gly	Ser	Glu
			245						250					255	
Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Ser	His	His	His	His	His
		260						265					270		

His

<210> 4
 <211> 35
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen
 Sequenz: Primer

<400> 4
 cagccggcca tggcgcaggt cgcagctgca gcgag

35

<210> 5
 <211> 38
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen
 Sequenz: Primer

<400> 5
 ccagggggcca gtggatagac aagcttgggt gttgtttt

38

<210> 6
 <211> 30
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen
 Sequenz: Primer

<400> 6

agagacgcgt acaggctggt gtgactcagg

30

<210> 7
 <211> 27
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen
 Sequenz: Primer

<400> 7

gactgcgccc gcagacttgg gctggcc

27

<210> 8
 <211> 21
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen
 Sequenz: Primer

<400> 8

atgaccatga ttacgccaag c

21

<210> 9
 <211> 36
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen
 Sequenz: Primer

<400> 9

agacaagctt ggggtgttgg ttggctgagg agacgg

36

<210> 10
 <211> 27
 <212> DNA
 <213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen
Sequenz: Primer

<400> 10

ggcggatatc gagctcactc agtctcc

27

<210> 11

<211> 34

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen
Sequenz: Primer

<400> 11

tatagcggcc gcagcatcag cccgtttgat ttcc

34